

Sequence Listing

SEQUENCE LISTING

<110> Steinkasserer, Alexander

<120> Use of Soluble Forms of CD83 and Nucleic Acids Encoding them for the Treatment or Prevention of Diseases

<130> 032723woJH

<140>

<141>

<160> 12

<170> PatentIn Ver. 2.1

<210> 1

<211> 618

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(615)

<400> 1

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1 5 10 15	
gct ccc gcg acg ccg gag gtg aag gtg gct tgc tcc gaa gat gtg gac	96
Ala Pro Ala Thr Pro Glu Val Lys Val Ala Cys Ser Glu Asp Val Asp	
20 25 30	
ttg ccc tgc acc gcc ccc tgg gat ccg cag gtt ccc tac acg gtc tcc	144
Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Val Pro Tyr Thr Val Ser	
35 40 45	
tgg gtc aag tta ttg gag ggt ggt gaa gag agg atg gag aca ccc cag	192
Trp Val Lys Leu Leu Glu Gly Gly Glu Glu Arg Met Glu Thr Pro Gln	
50 55 60	
gaa gac cac ctc agg gga cag cac tat cat cag aag ggg caa aat ggt	240
Glu Asp His Leu Arg Gly Gln His Tyr His Gln Lys Gly Gln Asn Gly	
65 70 75 80	
tct ttc gac gcc ccc aat gaa agg ccc tat tcc ctg aag atc cga aac	288
Ser Phe Asp Ala Pro Asn Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn	
85 90 95	
act acc agc tgc aac tgc ggg aca tac agg tgc act ctg cag gac ccg	336
Thr Thr Ser Cys Asn Ser Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro	
100 105 110	
gat ggg cag aga aac cta agt ggc aag gtg atc ttg aga gtg aca gga	384
Asp Gly Gln Arg Asn Leu Ser Gly Lys Val Ile Leu Arg Val Thr Gly	
115 120 125	
tgc cct gca cag cgt aaa gaa gag act ttt aag aaa tac aga gcg gag	432
Cys Pro Ala Gln Arg Lys Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu	
130 135 140 145	
att gtc ctg ctg ctg gct ctg gtt att ttc tac tta aca ctc atc att	480
Ile Val Leu Leu Leu Ala Leu Val Ile Phe Tyr Leu Thr Leu Ile Ile	
150 155 160	
ttc act tgt aag ttt gca cgg cta cag agt atc ttc cca gat ttt tct	528

phe Thr Cys Lys Phe Ala Arg Leu Gln Ser Ile phe Pro Asp phe Ser
165 170 175

aaa gct ggc atg gaa cga gct ttt ctc cca gtt acc tcc cca aat aag 576
Lys Ala Gly Met Glu Arg Ala Phe Leu Pro Val Thr Ser Pro Asn Lys
180 185 190

cat tta ggg cta gtg act cct cac aag aca gaa ctg gta tga 618
His Leu Gly Leu Val Thr Pro His Lys Thr Glu Leu Val
195 200 205

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<210> 2
<211> 205
<212> PRT
<213> Homo sapiens
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<400> 2
Met Ser Arg Gly Leu Gln Leu Leu Leu Ser Cys Ala Tyr Ser Leu
1 5 10 15

Ala Pro Ala Thr Pro Glu Val Lys Val Ala Cys Ser Glu Asp Val Asp

Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Val Pro Tyr Thr Val Ser
35 40 45

Trp Val Lys Leu Leu Glu Gly Gly Glu Glu Arg Met Glu Thr Pro Gln
50 55 60

Glu Asp His Leu Arg Gly Gln His Tyr His Gln Lys Gly Gln Asn Gly
65 70 75 80

Ser Phe Asp Ala Pro Asn Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn
85 90 95

Thr Thr Ser Cys Asn Ser Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro
100 105 110

Asp Gly Gln Arg Asn Leu Ser Gly Lys Val Ile Leu Arg Val Thr Gly
115 120 125

Cys Pro Ala Gln Arg Lys Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu
130 135 140

Ile Val Leu Leu Leu Ala Leu Val Ile Phe Tyr Leu Thr Leu Ile Ile
145 150 155 160

Phe Thr Cys Lys Phe Ala Arg Leu Gln Ser Ile Phe Pro Asp Phe Ser
165 170 175

Lys Ala Gly Met Glu Arg Ala Phe Leu Pro Val Thr Ser Pro Asn Lys
180 185 190

His Leu Gly Leu Val Thr Pro His Lys Thr Glu Leu Val
195 200 205

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<210> 3
<211> 2051
<212> DNA
<213> Mus musculus
<220>
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Sequence Listing

<221> CDS

<222> (14)..(601)

<400> 3

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      Met Ser Gln Gly Leu Gln Leu Leu Phe Leu Gly Cys
      1          5          10

gcc tgc agc ctg gca ccc gcg atg gcg atg cgg gag gtg acg gtg gct 97
Ala Cys Ser 15 Leu Ala Pro Ala Met Ala Met Arg Glu Val Thr Val Ala
      20          25

tgc tcc gag acc gcc gac ttg cct tgc aca gcg ccc tgg gac ccg cag 145
Cys Ser 30 Glu Thr Ala Asp Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln
      35          40

ctc tcc tat gca gtg tcc tgg gcc aag gtc tcc gag agt ggc act gag 193
Leu Ser Tyr Ala Val Trp 50 Trp Ala Lys Val Ser 55 Glu Ser Gly Thr Glu 60
      45          50          55          60

agt gtg gag ctc ccg gag agc aag caa aac agc tcc ttc gag gcc ccc 241
Ser Val Glu Leu Pro Glu Ser Lys Gln Asn Ser Ser Phe Glu Ala Pro 75
      65          70          75

agg aga agg gcc tat tcc ctg acg atc caa aac act acc atc tgc agc 289
Arg Arg Arg Ala Tyr Ser Leu Thr Ile Gln Asn Thr Thr Ile Cys Ser 85
      80          85          90

tcg ggc acc tac agg tgt gcc ctg cag gag ctc gga ggg cag cgc aac 337
Ser Gly Thr Tyr Arg Cys Ala Leu Gln Glu Leu Gly Gly Gln Arg Asn 105
      95          100          105

ttg agc ggc acc gtg gtt ctg aag gtg aca gga tgc ccc aag gaa gct 385
Leu Ser 110 Gly Thr Val Val Leu Lys Val Thr Gly Cys Pro Lys Glu Ala 115
      110          115          120

aca gag tca act ttc agg aag tac agg gca gaa gct gtg ttg ctc ttc 433
Thr Glu Ser Thr Phe Arg Lys Tyr Arg Ala Glu Ala Val Leu Leu Phe 135
      125          130          135          140

tct ctg gtt gtt ttc tac ctg aca ctc atc att ttc acc tgc aaa ttt 481
Ser Leu Val Val Phe Tyr Leu Thr Leu Ile Ile Phe Thr Cys Lys Phe 145
      145          150          155

gca cga cta caa agc att ttc cca gat att tct aaa cct ggt acg gaa 529
Ala Arg Leu Gln Ser Ile Phe Pro Asp Ile Ser Lys Pro Gly Thr Glu 160
      160          165          170

caa gct ttt ctt cca gtc acc tcc cca agc aaa cat ttg ggg cca gtg 577
Gln Ala Phe 175 Leu Pro Val Thr Ser Pro Ser Lys His Leu Gly Pro Val 180
      175          180          185

acc ctt cct aag aca gaa acg gta tgagtaggat ctccactggt ttttacaag 631
Thr Leu Pro Lys Thr Glu Thr Val 190
      190

ccaagggcac atcagatcag tgtgcctgaa tgccaccgg acaagagaag aatgagctcc 691
atcctcagat ggcaaccttt ctttgaagtc cttcacctga cagtgggctc cacactactc 751
cctgacacag ggtcttgagc accatcatat gatcacgaag catggagtat caccgctttc 811

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Sequence Listing

ctgtggctgt cagcttaaat ttctcatgtg ctatctggtc aacctctgta gtgcttttca 871
 gtcatctaca agctatggtg agatgcaggt gaagcagggt catgggaaat ttgaacactc 931
 tgagctggcc ctgtgacaga ctctgagga cagctgtcct ctctacatc tgggatacat 991
 ctctttgaat ttgtcctgtt tcgttgacc agcccatgt tctcacatct ggcggaaatt 1051
 gacaggccaa gctgtgacc agtgggaaat atttagcaaa taatttccca gtgcgaagggt 1111
 cctgctatta gtaaggagta ttatgtgtac atagaaatga gaggtcagtg aactattccc 1171
 cagcagggcc ttttcatctg gaaaagacat ccacaaaagc agcaatacag agggatgcc 1231
 catttatttt tttaattctt atgtacttgt caaagaagaa tttttcatgt tttttcaag 1291
 aagtgtgttt ctttctttt ttaaaatatg aaggcttagt tacatagcat tgctagctga 1351
 caagcagcct gagagaagat ggagaatgtt ctccaaata gggacagcaa gctagaagca 1411
 ctgtacagtg cctgctggg aagggcagac aatggactga gaaaccagaa gtctggccac 1471
 aagattgtct gtatgattct ggacgagtc ctgtgtgtt tcactctctg gtagtaaac 1531
 cagatagttt agtctgggtt gaatacaatg gatgtgaagt tgcttgggga aagctgaatg 1591
 tagtgaatac attggcaact ctactgggct gttaccttgt tgatataccta gagttctgga 1651
 gctgagcgaa tgctgtcat atctcagctt gcccatcaat ccaaacacag gaggtcaca 1711
 aaaggacatg agcatggctt tctgtgtgaa ctctctctga gaaacgtgga gactggctca 1771
 gcgcttttgc cttgaaggac taatcacaag ttcttgaaga tatggaccta ggggagctat 1831
 tgcgccacga caggaggaag ttctcagatg ttgcattgat gtaacattgt tgcatattct 1891
 taatgagctg ggctccttcc tcatttgctt ccaaaagaga ttttgctcca ctaattggtg 1951
 gcccatcacc cacactatga aagtaaaagg gatgctgagc agatacagcg tgcttacctc 2011
 tcagccatga ctttcatgct attaaaaagaa tgcatgtgaa 2051

<210> 4
 <211> 196
 <212> PRT
 <213> Mus musculus

<400> 4
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 1 5 10 15
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 20 25 30
 Ala Asp Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Leu 45 Ser Tyr Ala
 35 40 45
 Val Ser Trp Ala Lys Val Ser Glu Ser Gly Thr Glu Ser Val Glu Leu
 50 55 60
 Pro Glu Ser Lys Gln Asn Ser Ser Phe Glu Ala Pro Arg Arg Arg Ala

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65		70		75		80
Tyr	Ser	Leu	Thr	Ile	Gln	Asn
				85		Thr
						Thr
						90
						Cys
						Ser
						Ser
						Gly
						Thr
						95
Arg	Cys	Ala	Leu	Gln	Glu	Leu
						Gly
						100
						Gly
						105
						Gln
						Arg
						Asn
						Leu
						Ser
						Gly
						Thr
						110
Val	Val	Leu	Lys	Val	Thr	Gly
						Cys
						115
						Pro
						Lys
						Glu
						Ala
						Thr
						Glu
						Ser
						Thr
						120
Phe	Arg	Lys	Tyr	Arg	Ala	Glu
						Ala
						Val
						Leu
						Leu
						Phe
						Ser
						Leu
						Val
						Val
						130
Phe	Tyr	Leu	Thr	Leu	Ile	Ile
						Phe
						Thr
						Cys
						Lys
						135
						Phe
						Ala
						Arg
						Leu
						Gln
						140
Phe	Tyr	Leu	Thr	Leu	Ile	Ile
						Phe
						Thr
						Cys
						Lys
						145
						Phe
						Ala
						Arg
						Leu
						Gln
						150
Ser	Ile	Phe	Pro	Asp	Ile	Ser
						Lys
						Pro
						Gly
						Thr
						Glu
						Gln
						Ala
						Phe
						Leu
						155
						Gly
						Thr
						Glu
						Gln
						Ala
						Phe
						Leu
						160
Pro	Val	Thr	Ser	Pro	Ser	Lys
						His
						Leu
						Gly
						Pro
						Val
						Thr
						Leu
						Pro
						Lys
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						Leu
						175
						Gly
						Thr
						Glu
						Gln
						Ala
						Phe
						Leu
						180
						Gly
						Thr
						Leu
						Pro
						Lys
						185
						Gly
						Thr
						Leu
						Pro
						Lys
						190
						Gly
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						195
						Gly
						Thr
						Leu
						Pro
						Lys
						200

<210> 5
 <211> 31
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: primer for CD83ext

<400> 5
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<210> 6
 <211> 31
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: primer for CD83ext

<400> 6
 aattagaatt ctcaaatctc cgctctgtat t 31

<210> 7
 <211> 435
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: partial
 sequence of pGEX2ThCD83ext
 <220>
 <221> CDS
 <222> (1)..(417)
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 <221> mat_peptide
 <222> (28)..(417)

Sequence Listing

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Pro Pro Lys Ser Asp -5 Leu Val Pro Arg -1 Gly 1 Ser Pro Gly 5 Pro Pro Glu

gtg aag gtg gct tgc tcc gaa gat gtg gac ttg ccc tgc acc gcc ccc 96
Val Lys Val 10 Ala Cys Ser Glu Asp 15 Val Asp Leu Pro Cys 20 Thr Ala Pro

tgg gat ccg cag gtt ccc tac acg gtc tcc tgg gtc aag tta ttg gag 144
Trp Asp 25 Pro Gln Val Pro Tyr 30 Thr Val Ser Trp 35 Val Lys Leu Leu Glu

ggt ggt gaa gag agg atg gag aca ccc cag gaa gac cac ctc agg gga 192
Gly Gly Glu Glu Arg Met 45 Glu Thr Pro Gln Glu 50 Asp His Leu Arg Gly 55

cag cac tat cat cag aag ggg caa aat ggt tct ttc gac gcc ccc aat 240
Gln His Tyr His Gln Lys Gly Gln Asn Gly 65 Ser Phe Asp Ala Pro Asn 70

gaa agg ccc tat tcc ctg aag atc cga aac act acc agc tgc aac tcg 288
Glu Arg Pro Tyr 75 Ser Leu Lys Ile Arg 80 Asn Thr Thr Ser Cys 85 Asn Ser

ggg aca tac agg tgc act ctg cag gac ccg gat ggg cag aga aac cta 336
Gly Thr Tyr Arg Cys Thr Leu Gln 95 Asp Pro Asp Gly 100 Gln Arg Asn Leu 90

agt ggc aag gtg atc ttg aga gtg aca gga tgc cct gca cag cgt aaa 384
Ser Gly Lys Val Ile Leu Arg 110 Val Thr Gly Cys Pro 115 Ala Gln Arg Lys 105

gaa gag act ttt aag aaa tac aga gcg gag att tgagaattca tcgtgact 435
Glu Glu Thr Phe Lys Lys 125 Tyr Arg Ala Glu Ile 130

<210> 8
<211> 139
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: partial
sequence of pGEX2ThCD83ext

<400> 8
Pro Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Pro Gly Thr Pro Glu
-5 -1 1 5

Val Lys Val Ala Cys Ser Glu Asp Val Asp Leu Pro Cys Thr Ala Pro
10 15 20

Trp Asp Pro Gln Val Pro Tyr Thr Val Ser Trp Val Lys Leu Leu Glu
25 30 35

Gly Gly Glu Glu Arg Met Glu Thr Pro Gln Glu Asp His Leu Arg Gly
40 45 50 55

Gln His Tyr His Gln Lys Gly Gln Asn Gly Ser Phe Asp Ala Pro Asn
60 65 70

Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn Thr Thr Ser Cys Asn Ser
75 80 85

Sequence Listing

Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro Asp Gly Gln Arg Asn Leu
 90 95 100
 Ser Gly Lys Val Ile Leu Arg Val Thr Gly Cys Pro Ala Gln Arg Lys
 105 110 115
 Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu Ile
 120 125 130

<210> 9
 <211> 435
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: partial
 sequence of pGEX2ThCD83ext_mut129_CtoS
 <220>
 <221> CDS
 <222> (1)..(417)
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 <221> mat_peptide
 <222> (28)..(417)

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 Pro Pro Lys Ser Asp -5 Leu Val Pro -1 1 Ser Pro Gly Thr Pro Glu
 gtg aag gtg gct tgc tcc gaa gat gtg gac ttg ccc tgc acc gcc ccc 96
 Val Lys Val Ala Cys Ser Glu Asp Val Asp Leu Pro Cys Thr Ala Pro
 10 15 20
 tgg gat ccg cag gtt ccc tac acg gtc tcc tgg gtc aag tta ttg gag 144
 Trp Asp Pro Gln Val Pro Tyr Thr Val Ser Trp Val Lys Leu Leu Glu
 25 30 35
 ggt ggt gaa gag agg atg gag aca ccc cag gaa gac cac ctc agg gga 192
 Gly Gly Glu Glu Arg Met Glu Thr Pro Gln Glu Asp His Leu Arg Gly
 40 45 50 55
 cag cac tat cat cag aag ggg caa aat ggt tct ttc gac gcc ccc aat 240
 Gln His Tyr His Gln Lys Gly Gln Asn Gly Ser Phe Asp Ala Pro Asn
 60 65 70
 gaa agg ccc tat tcc ctg aag atc cga aac act acc agc tgc aac tcg 288
 Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn Thr Thr Ser Cys Asn Ser
 75 80 85
 ggg aca tac agg tgc act ctg cag gac ccg gat ggg cag aga aac cta 336
 Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro Asp Gly Gln Arg Asn Leu
 90 95 100
 agt ggc aag gtg atc ttg aga gtg aca gga tcc cct gca cag cgt aaa 384
 Ser Gly Lys Val Ile Leu Arg Val Thr Gly Ser Pro Ala Gln Arg Lys
 105 110 115
 gaa gag act ttt aag aaa tac aga gcg gag att tgagaattca tcgtgact 435
 Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu Ile
 120 125 130

Sequence Listing

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<210> 10
<211> 139
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: partial
        sequence of pGEX2ThCD83ext_mut129_CtoS

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      -5      -1      1      5
Val Lys Val Ala Cys Ser Glu Asp Val Asp Leu Pro Cys Thr Ala Pro
      10      15      20
Trp Asp Pro Gln Val Pro Tyr Thr Val Ser Trp Val Lys Leu Leu Glu
      25      30      35
Gly Gly Glu Glu Arg Met Glu Thr Pro Gln Glu Asp His Leu Arg Gly
      40      45      50      55
Gln His Tyr His Gln Lys Gly Gln Asn Gly Ser Phe Asp Ala Pro Asn
      60      65      70
Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn Thr Thr Ser Cys Asn Ser
      75      80      85
Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro Asp Gly Gln Arg Asn Leu
      90      95      100
Ser Gly Lys Val Ile Leu Arg Val Thr Gly Ser Pro Ala Gln Arg Lys
      105      110      115
Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu Ile
      120      125      130

<210> 11
<211> 32
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: primer
        sense-pGEX2ThCD83

<400> 11
tccccccggg aacgccggag gtgaaggtgg ct
                                     32

<210> 12
<211> 66
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: primer
        antisense-CD83extra_mutantCtoS

<400> 12
aattagaatt ctcaaatctc cgctctgtat ttcttaaaag tctcttcttt acgctgtgca 60
ggggat                                     66

<210> 13

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Sequence Listing

<211> 209

<212> PRT

<213> Homo sapiens

<400> 13

Gly Ser Pro Gly Met Ser Arg Gly Leu Gln Leu Leu Leu Ser Cys
1 5 10 15

Ala Tyr Ser Leu Ala Pro Ala Thr Pro Glu Val Lys Val Ala Cys Ser
20 25 30

Glu Asp Val Asp Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Val Pro
35 40 45

Tyr Thr Val Ser Trp Val Lys Leu Leu Glu Gly Glu Glu Arg Met
50 55 60

Glu Thr Pro Gln Glu Asp His Leu Arg Gly Gln His Tyr His Gln Lys
65 70 75 80

Gly Gln Asn Gly Ser Phe Asp Ala Pro Asn Glu Arg Pro Tyr Ser Leu
85 90 95

Lys Ile Arg Asn Thr Thr Ser Cys Asn Ser Gly Thr Tyr Arg Cys Thr
100 105 110

Leu Gln Asp Pro Asp Gly Gln Arg Asn Leu Ser Gly Lys Val Ile Leu
115 120 125

Arg Val Thr Gly Cys Pro Ala Gln Arg Lys Glu Glu Thr Phe Lys Lys
130 135 140

Arg Arg Ala Glu Ile Val Leu Leu Leu Ala Leu Val Ile Phe Tyr Leu
145 150 155 160

Thr Leu Ile Ile Phe Thr Cys Lys Phe Ala Arg Leu Gln Ser Ile Phe
165 170 175

Pro Asp Phe Ser Lys Ala Gly Met Glu Arg Ala Phe Leu Pro Val Thr
180 185 190

Ser Pro Asn Lys His Leu Gly Leu Val Thr Pro His Lys Thr Glu Leu
195 200 205

Val
209